

PCTA9407-2(한국생명공학연구원)

<110> Korea Research Institute of Bioscience and Biotechnology

<120> A novel Hansenula polymorpha gene coding for alpha 1,6 mannosyltransferase and process for the production of recombinant glycoproteins with Hansenula polymorpha mutant strain deficient in the same gene

<160> 14

<170> KopatentIn 1.71

<210> 1

<211> 1351

<212> DNA

<213> Hansenula polymorpha

<220>

<221> CDS

<222> (10)..(1293)

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	1				5					10							
gtg	ctg	aag	cgc	gcg	cga	ctc	tac	atg	gcg	acg	aat	cgc	cgg	ctg	gtg		99
Val	Leu	Lys	Arg	Ala	Arg	Leu	Tyr	Met	Ala	Thr	Asn	Arg	Arg	Leu	Val		
15				20					25					30			
ggt	gtt	ctt	gtg	gtg	ctg	ctg	tac	tgg	gtg	gtc	cag	aac	gtt	tgg	acg		147
Val	Val	Leu	Val	Val	Leu	Leu	Tyr	Trp	Val	Val	Gln	Asn	Val	Trp	Thr		
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tgg	agc	cct	ggg	acg	cgc	gat	ttg	gcc	caa	gtg	gac	gcg	aag	atc	gag		195
Trp	Ser	Pro	Gly	Thr	Arg	Asp	Leu	Ala	Gln	Val	Asp	Ala	Lys	Ile	Glu		
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gcc	gag	cta	aac	tcg	aat	cta	cat	act	ttt	gga	gcg	cat	ttg	cgc	cac		243
Ala	Glu	Leu	Asn	Ser	Asn	Leu	His	Thr	Phe	Gly	Ala	His	Leu	Arg	His		
	65					70						75					
tta	aac	cgg	ctt	cgg	gca	gag	tcg	gcc	acc	ctg	cgt	gaa	aaa	ctc	acc		291
Leu	Asn	Arg	Leu	Pro	Ala	Glu	Ser	Ala	Thr	Leu	Arg	Glu	Lys	Leu	Thr		
	80				85					90							
ttc	tat	ttc	cca	tat	tat	cct	gaa	aag	ccc	gtg	cgg	aac	cag	atc	tgg		339
Phe	Tyr	Phe	Pro	Tyr	Tyr	Pro	Glu	Lys	Pro	Val	Pro	Asn	Gln	Ile	Trp		
95					100					105				110			
cag	aca	tgg	aag	gtc	gat	ctc	gaa	gac	gac	aac	ttc	ccc	aag	cag	tac		387
Gln	Thr	Trp	Lys	Val	Asp	Leu	Glu	Asp	Asp	Asn	Phe	Pro	Lys	Gln	Tyr		
			115					120						125			
aga	cgg	ttt	cag	aag	acg	tgg	gtc	gag	aaa	aat	cca	gac	tac	gtg	tac		435
Arg	Arg	Phe	Gln	Lys	Thr	Trp	Val	Glu	Lys	Asn	Pro	Asp	Tyr	Val	Tyr		
	130							135					140				
cac	ctg	att	cgg	gac	tct	gtg	att	gag	gac	ttt	gtg	gcg	agt	ttg	tac		483
His	Leu	Ile	Pro	Asp	Ser	Val	Ile	Glu	Asp	Phe	Val	Ala	Ser	Leu	Tyr		
	145					150					155						
gcg	aac	gtg	cgg	gag	gtg	gtc	aga	gcg	tac	cag	ctg	ctt	cgg	aaa	aat		531
Ala	Asn	Val	Pro	Glu	Val	Val	Arg	Ala	Tyr	Gln	Leu	Leu	Pro	Lys	Asn		
	160				165						170						
atc	atg	aag	gcg	gat	ttt	ttc	cgg	tat	ttg	gtg	atc	tac	gcg	cgc	gga		579
Ile	Met	Lys	Ala	Asp	Phe	Phe	Arg	Tyr	Leu	Val	Ile	Tyr	Ala	Arg	Gly		
175					180				185					190			
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Gly	Thr	Tyr	Ser	Asp	Met	Asp	Thr	Val	Cys	Leu	Lys	Pro	Ile	Lys	Asp		
			195					200						205			
tgg	gcc	acg	ttt	gat	cgc	gac	ctg	atc	cac	gct	gcc	gac	aat	aag	gcc		675
Trp	Ala	Thr	Phe	Asp	Arg	Asp	Leu	Ile	His	Ala	Ala	Asp	Asn	Lys	Ala		

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210	215	220	
gat ctc tcc cag ata gat cca gaa gca aga acc acg cct gtg ggg ctg Asp Leu Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu 225 230 235			723
gtg att ggc att gag gcc gac ccg gac agg ccc gac tgg cac gag tgg Val Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp 240 245 250			771
ttc tgc cgc aga ctg cag ttc tgc cag tgg acg atc cag gcg aag ccg Phe Ser Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro 255 260 265 270			819
gga cac ccg ctg ctg cgc gag ctg atc atc ccg atc gtg gag gag acg Gly His Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr 275 280 285			867
ttc cgc aaa cag cac atg ggc gtt ttg aaa aga gtg gaa ggc aag gac Phe Arg Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp 290 295 300			915
tcg ggc gca gat atc atg cag tgg aca gga ccg ggg ata ttt aca gac Ser Gly Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp 305 310 315			963
act ctg ttt gat tat ctg aac aat gtg gcg agc gac ggc aag ttg ggc Thr Leu Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly 320 325 330			1011
gac ggg tac ggc gtg ggg tgc ttg tat tgg cgc aag cac ggc aaa tat Asp Gly Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr 335 340 345 350			1059
aag ctg aaa aag aca gaa att aac aag aat aac gag cca ttg cat tct Lys Leu Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser 355 360 365			1107
gag gac cag ctt atc aac tgg agg tgc ctg acc aac atg gac aag cca Glu Asp Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro 370 375 380			1155
aag atc atg ggc gac gta atg gtg tta cca atc acg agc ttt agt ccg Lys Ile Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro 385 390 395			1203
aac gtg ggc cac atg ggc tca aag agc agc tca gat agg ctg gca ttt Asn Val Gly His Met Gly Ser Lys Ser Ser Ser Asp Arg Leu Ala Phe 400 405 410			1251
gtg gag cat tta ttt tct ggc agc tgg aag cca aaa aac aaa taggaaa Val Glu His Leu Phe Ser Gly Ser Trp Lys Pro Lys Asn Lys 415 420 425			1300
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Lys Arg Ala Arg Leu Tyr Met Ala Thr Asn Arg Arg Leu Val Val Val  
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Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr Trp Ser  
35 40 45  
Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu Ala Glu  
50 55 60

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Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His Leu Asn  
 65 70 75 80  
 Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr Phe Tyr  
 85 90 95  
 Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr  
 100 105 110  
 Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr Arg Arg  
 115 120 125  
 Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr His Leu  
 130 135 140  
 Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr Ala Asn  
 145 150 155 160  
 Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn Ile Met  
 165 170 175  
 Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly Gly Thr  
 180 185 190  
 Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp Trp Ala  
 195 200 205  
 Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala Asp Leu  
 210 215 220  
 Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu Val Ile  
 225 230 235 240  
 Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp Phe Ser  
 245 250 255  
 Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro Gly His  
 260 265 270  
 Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr Phe Arg  
 275 280 285  
 Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp Ser Gly  
 290 295 300  
 Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp Thr Leu  
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 Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly Asp Gly  
 325 330 335  
 Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr Lys Leu  
 340 345 350  
 Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser Glu Asp  
 355 360 365  
 Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro Lys Ile  
 370 375 380  
 Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro Asn Val  
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